

Amendments to the Claims:

The following list of claims will replace all prior versions of the claims in the application:

1. (*Currently amended*) A computer-implemented method for identifying patterns in data, the method comprising:

(a) inputting into ~~a classifier~~ at least one support vector machine of a plurality of support vector machines a training set having known outcomes, the ~~classifier~~ at least one support vector machine comprising a decision function having a plurality of weights, each having a weight value, wherein the training set comprises features corresponding to the data and wherein each feature has a corresponding weight;

(b) optimizing the plurality of weights so that classifier error is minimized;

(c) computing ranking criteria using the optimized plurality of weights;

(d) eliminating at least one feature corresponding to the smallest ranking criterion;

(e) repeating steps (a) through (d) for a plurality of iterations until a subset of features of pre-determined size remains; and

(f) inputting into the ~~classifier~~ at least one support vector machine a live set of data wherein the features within the live set are selected according to the subset of features.

2. (*Canceled*)

3. (*Currently amended*) The method of claim 1, wherein the ~~classifier~~ at least one support vector machine is a soft margin support vector machine.

4. (*Original*) The method of claim 1, wherein the ranking criterion corresponding to a feature is calculated by squaring the optimized weight for the corresponding feature.

5. (*Original*) The method of claim 1, wherein the decision function is a quadratic function.

6. (*Original*) The method of claim 1, wherein step (d) comprises eliminating a plurality of features corresponding to the smallest ranking criteria in a single iteration of steps (a) through (d).

7. (*Original*) The method of claim 1, wherein step (d) comprises eliminating a plurality of features corresponding to the smallest ranking criteria in at least the first iteration of steps (a) through (d) and in later iterations, eliminating one feature for each iteration.

8. (*Original*) The method of claim 1, wherein step (d) comprises eliminating a plurality of features corresponding to the smallest ranking criteria so that the number of features is reduced by a factor of two for each iteration.

9. (*Original*) The method of claim 1, wherein the training set and the live set each comprise gene expression data obtained from DNA micro-arrays.

10. (*Original*) The method of claim 1, further comprising pre-processing the training set and the live set so that the features are comparably scaled.

11. (*New*) The method of claim 1, wherein step (e) further comprises using a new support vector machine for each iteration.

12. (*New*) The method of claim 1, further comprising the steps of:
pre-processing the training data set using unsupervised clustering to generate a plurality of data clusters;
selecting a cluster center from each of a plurality of data clusters;
using the cluster centers to perform steps (b) to (e).

13. (*New*) The method of claim 1, further comprising, after step (e), post-processing the optimum subset of features to generate a plurality of clusters, wherein each feature in the optimum subset of features is a cluster center.

14. (*New*) A computer-implemented method for identifying determinative genes for use in diagnosis, prognosis or treatment of a disease, the method comprising:

(a) inputting into a support vector machine a training data set of gene expression data having known outcomes with respect to the disease, the support vector machine comprising a decision function having a plurality of weights, each having a weight value, wherein the training set comprises features corresponding to the gene expression data and each feature has a corresponding weight;

(b) optimizing the plurality of weights so that classifier error is minimized;

(c) computing ranking criteria using the optimized plurality of weights;

(d) eliminating at least one feature corresponding to the smallest ranking criterion;

(e) repeating steps (a) through (d) for a plurality of iterations until an optimum subset of features remains; and

(f) inputting into the support vector machine a live data set of gene expression data wherein the features within the live data set are selected according to the optimum subset of features.

15. (*New*) The method of claim 14, wherein step (d) comprises eliminating a plurality of features corresponding to the smallest ranking criteria in a single iteration of steps (a) through (d).

16. (*New*) The method of claim 14, wherein step (d) comprises eliminating a plurality of features corresponding to the smallest ranking criteria in at least the first iteration of steps (a) through (d) and in later iterations, eliminating one feature for each iteration.

17. (New) The method of claim 14, wherein step (d) comprises eliminating a plurality of features corresponding to the smallest ranking criteria so that the number of features is reduced by a factor of two for each iteration.

18. (New) The method of claim 14, wherein step (e) further comprises using a new support vector machine for each iteration.

19. (New) The method of claim 14, further comprising pre-processing the training set to decrease skew in the data distribution.

20. (New) A computer-implemented method for identifying patterns in biological data, the method comprising:

(a) inputting into at least some of a plurality of support vector machines a training data set, wherein the training data set comprises features corresponding to the biological data and each feature has a corresponding weight, and wherein each support vector machine comprises a decision function having a plurality of weights;

(b) optimizing the plurality of weights so that classification confidence is optimized;

(c) computing ranking criteria using the optimized plurality of weights;

(d) eliminating at least one feature corresponding to the smallest ranking criteria;

(e) repeating steps (a) through (d) for a plurality of iterations until an optimum subset of features remains; and

(f) inputting into the plurality of support vector machines a live set of biological data wherein the features within the live set are selected according to the optimum subset of features.

21. (New) The method of claim 20, wherein step (e) further comprises using a new support vector machine for each iteration.

22. (*New*) The method of claim 20, wherein step (d) comprises eliminating a plurality of features corresponding to the smallest ranking criteria in a single iteration of steps (a) through (d).

23. (*New*) The method of claim 20, wherein step (d) comprises eliminating a plurality of features corresponding to the smallest ranking criteria in at least the first iteration of steps (a) through (d) and in later iterations, eliminating one feature for each iteration.

24. (*New*) The method of claim 20, wherein step (d) comprises eliminating a plurality of features corresponding to the smallest ranking criteria so that the number of features is reduced by a factor of two for each iteration.